

570  
/2/1

#8

OIPE

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/932,227

DATE: 12/03/2001  
 TIME: 10:52:53

Input Set : A:\58715-A-PCT-US.txt  
 Output Set: N:\CRF3\11212001\I932227.raw

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3 <110> APPLICANT: VOSSHALL, LESLIE
4   AMREIN, HUBERT
5   AXEL, RICHARD
7 <120> TITLE OF INVENTION: GENES ENCODING INSECT ODORANT RECEPTORS AND USES THEREOF
9 <130> FILE REFERENCE: 0575/58715-A-PCT-US/JPW/ADM/BJA
11 <140> CURRENT APPLICATION NUMBER: US 09/932,227
12 <141> CURRENT FILING DATE: 2001-08-17
14 <150> PRIOR APPLICATION NUMBER: PCT/US00/04995
15 <151> PRIOR FILING DATE: 2000-02-25
17 <160> NUMBER OF SEQ ID NOS: 108
19 <170> SOFTWARE: PatentIn version 3.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1285
23 <212> TYPE: DNA
24 <213> ORGANISM: DROSOPHILA MELANOGASTER DOR62
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29 gtttgggagc tcaactggcct gatgcgtcct ccgggcggtt caagcctgct ttacgtggta      120
31 tactccaatta cgggtcaactt ggtgggtcacc gtgctgtttc ccttgagctt gctggccagg      180
33 ctgctgttca ccaccaacat gcccggtattg tgcgagaacc tgaccataac tattaccgat      240
35 attgtggcca atttgaagtt tgcgaatgtg tacatggtga ggaagcagct ccatgagatt      300
37 cgctctctcc taaggctcat ggacgctaga gcccggtctg tgggcgatcc cgaggagatt      360
39 tctgccttga ggaaggaagt gaatategca cagggcactt tccgcacctt tgccagtatt      420
41 ttcgtatttg gcactacttt gagttgcgtc cgcgtggtcg ttgcgccgga tcgagagctc      480
43 ctgtatccgg cctggtttcgg cgttgactgg atgcactcca ccagaaacta tgtgctcatc      540
45 aatatctacc agctcttcgg cttgatagtg caggctatac agaactgcgc tagtgactcc      600
47 tatccgctcg cgtttctctg cctgctcacg ggtcatatgc gtgctttgga gctgaggggtg      660
49 cggcgattg gctgcaggac ggaaaaagtc aataaagggc agacatatga agcctggcgg      720
51 gaggaggtgt accaggaact catcgagtgc atccgcgcatc tggcgcggtt ccacgcgctg      780
53 agggagatca ttcagcgggt cctttcagtg ccttgcattg ccaggttcgt ctgctccgcc      840
55 gccgtccagt gtaccgtcgc catgcacttc ctgtacgtag cggatgacca cgaccacacc      900
57 gccatgatca tctcgattgt atttttctcg gccgtcacct tggagggtgt tgtaactctgc      960
59 tattttgggg acaggatgag gacacagagc gaggcgctgt gcgatgcctt ctacgattgc      1020
61 aactggatag aacagctgcc caagtccaag cgcgaactgc tcttcaacct gccaggagac      1080
63 cagcggcctt ctcttattta cgcaggcaac tacatcgcac tctcgttgga gaccttcgag      1140
65 caggtcatga ggttcacata ctctgttttc acactcttgc tgagggccaa gtaagaactt      1200
67 tataatctct ttttggggag aaaaatttta aagcacaata gcagaaaaat atatcagata      1260
69 atataacaaa aaaaaaaaaa aaaaaa      1285
72 <210> SEQ ID NO: 2
73 <211> LENGTH: 397
74 <212> TYPE: PRT
75 <213> ORGANISM: DROSOPHILA MELANOGASTER DOR62
77 <400> SEQUENCE: 2
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80 1          5          10          15
82 Tyr His Trp Arg Val Trp Glu Leu Thr Gly Leu Met Arg Pro Pro Gly
83          20          25          30

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85 Val Ser Ser Leu Leu Tyr Val Val Tyr Ser Ile Thr Val Asn Leu Val
86      35      40      45
88 Val Thr Val Leu Phe Pro Leu Ser Leu Leu Ala Arg Leu Leu Phe Thr
89      50      55      60
91 Thr Asn Met Ala Gly Leu Cys Glu Asn Leu Thr Ile Thr Ile Thr Asp
92 65      70      75      80
94 Ile Val Ala Asn Leu Lys Phe Ala Asn Val Tyr Met Val Arg Lys Gln
95      85      90      95
97 Leu His Glu Ile Arg Ser Leu Leu Arg Leu Met Asp Ala Arg Ala Arg
98      100      105      110
100 Leu Val Gly Asp Pro Glu Glu Ile Ser Ala Leu Arg Lys Glu Val Asn
101      115      120      125
103 Ile Ala Gln Gly Thr Phe Arg Thr Phe Ala Ser Ile Phe Val Phe Gly
104      130      135      140
106 Thr Thr Leu Ser Cys Val Arg Val Val Val Arg Pro Asp Arg Glu Leu
107 145      150      155      160
109 Leu Tyr Pro Ala Trp Phe Gly Val Asp Trp Met His Ser Thr Arg Asn
110      165      170      175
112 Tyr Val Leu Ile Asn Ile Tyr Gln Leu Phe Gly Leu Ile Val Gln Ala
113      180      185      190
115 Ile Gln Asn Cys Ala Ser Asp Ser Tyr Pro Pro Ala Phe Leu Cys Leu
116      195      200      205
118 Leu Thr Gly His Met Arg Ala Leu Glu Leu Arg Val Arg Arg Ile Gly
119      210      215      220
121 Cys Arg Thr Glu Lys Ser Asn Lys Gly Gln Thr Tyr Glu Ala Trp Arg
122 225      230      235      240
124 Glu Glu Val Tyr Gln Glu Leu Ile Glu Cys Ile Arg Asp Leu Ala Arg
125      245      250      255
127 Val His Arg Leu Arg Glu Ile Ile Gln Arg Val Leu Ser Val Pro Cys
128      260      265      270
130 Met Ala Gln Phe Val Cys Ser Ala Ala Val Gln Cys Thr Val Ala Met
131      275      280      285
133 His Phe Leu Tyr Val Ala Asp Asp His Asp His Thr Ala Met Ile Ile
134      290      295      300
136 Ser Ile Val Phe Phe Ser Ala Val Thr Leu Glu Val Phe Val Ile Cys
137 305      310      315      320
139 Tyr Phe Gly Asp Arg Met Arg Thr Gln Ser Glu Ala Leu Cys Asp Ala
140      325      330      335
142 Phe Tyr Asp Cys Asn Trp Ile Glu Gln Leu Pro Lys Phe Lys Arg Glu
143      340      345      350
145 Leu Leu Phe Thr Leu Ala Arg Thr Gln Arg Pro Ser Leu Ile Tyr Ala
146      355      360      365
148 Gly Asn Tyr Ile Ala Leu Ser Leu Glu Thr Phe Glu Gln Val Met Arg
149      370      375      380
151 Phe Thr Tyr Ser Val Phe Thr Leu Leu Leu Arg Ala Lys
152 385      390      395
154 <210> SEQ ID NO: 3
155 <211> LENGTH: 1499
156 <212> TYPE: DNA

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157 &lt;213&gt; ORGANISM: DROSOPHILA MELANOGASTER DOR104

159 &lt;400&gt; SEQUENCE: 3

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160 gaattcggca cgagcagtcg atggccagtc ttcagttcca cggaacgct gatgcggaca      60
162 tcaggtatga tattagcctg gatccggcta gggaatcgaa tctcttcctg ctgctaattgg    120
164 gactccagtt ggcgaatggc acgaagccat cgccgcggtt acccaaatgg tggccaaagc    180
166 ggctggaaat gattggtaaa gtgctgccca aagcctattg ttccatgggtg attttcacct    240
168 ccctgcattt ggtgtgctctg ttcacgaaaa ccacactgga tgtctgcgcg acggggggagc    300
170 tgcaggccat aacggatgcc ctcaccatga ccataatata ctttttcacg ggctacggca     360
172 ccatctactg gtgcctgcgc tcccggcgcc tcttggccta catggagcac atgaaccggg     420
174 agtatcgcca tcattcgctg gccgggggtga cctttgtgag tagccatgcg gcctttagga     480
176 tgtccagaaa cttcacggtg gtgtggataa tgtcctgcct gctgggcgtg atttctggg     540
178 gcgtttcgcc actgatgctg ggcacccgga tgtgcgcgct ccaatgttgg tatcccttcg     600
180 acgcctggg tcccggcaca tatacggcgg tctatgctac acaacttttc ggtcagatca     660
182 tgggtggcat gacctttgga ttcgggggat cactgtttgt caccctgagc ctgctactcc     720
184 tgggacaatt cgatgtgctc tactgcagcc tgaagaacct ggatgccat accaagttgc     780
186 tgggctggga gtctgtaaat ggctgagtt cgctgcaaga ggagtgtctg ctgggggact     840
188 cgaagaggga attaaatcag tacgttttgc tccaggagca tccgacggat ctgctgagat     900
190 tgtcggcagg acgaaaatgt cctgaccaag gaaatgcgtt tcacaacgcc ttggtggaat     960
192 gcattcgctt gcactgcctc attctgcact gctcacagga gtggagaat ctattcagtc    1020
194 catattgtct ggtcaagtca ctgcagatca cctttcagct ttgctgctg gtctttgtgg    1080
196 gcgtttcggg tactcgagag gtccctgcgga ttgtcaacca gctacagtac ttgggactga    1140
198 ccattctcga gtcctaatg ttcacctatt gtggcgaact cctcagtcgg catagtattc    1200
200 gatctggcga gccttttgg aggggtgcgt ggtggaagca cgccatttc atccgccagg    1260
202 acatcctcat ctttctggtc aatagtagac gtgcagttca cgtgactgcc ggcaagtttt    1320
204 atgtgatgga tgtgaatcgt taaagatcgg ttataacgca gccgttcagc ttcttgactt    1380
206 tgctgcaaaa gtggctgccc aagaagacgg aatcggagct ctaaaactgt acccgcac    1440
208 gatatttatt tagcgcatta aaaaaaagtc gagtaaaagc aaaaaaaaa aaaaaaaaa    1499

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211 &lt;210&gt; SEQ ID NO: 4

212 &lt;211&gt; LENGTH: 467

213 &lt;212&gt; TYPE: PRT

214 &lt;213&gt; ORGANISM: DROSOPHILA MELANOGASTER DOR104

216 &lt;400&gt; SEQUENCE: 4

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218 Met Ala Ser Leu Gln Phe His Gly Asn Val Asp Ala Asp Ile Arg Tyr
219 1      5      10      15
221 Asp Ile Ser Leu Asp Pro Ala Arg Glu Ser Asn Leu Phe Arg Leu Leu
222      20      25      30
224 Met Gly Leu Gln Leu Ala Asn Gly Thr Lys Pro Ser Pro Arg Leu Pro
225      35      40      45
227 Lys Trp Trp Pro Lys Arg Leu Glu Met Ile Gly Lys Val Leu Pro Lys
228      50      55      60
230 Ala Tyr Cys Ser Met Val Ile Phe Thr Ser Leu His Leu Gly Val Leu
231 65      70      75      80
233 Phe Thr Lys Thr Thr Leu Asp Val Leu Pro Thr Gly Glu Leu Gln Ala
234      85      90      95
236 Ile Thr Asp Ala Leu Thr Met Thr Ile Ile Tyr Phe Phe Thr Gly Tyr
237      100      105      110
239 Gly Thr Ile Tyr Trp Cys Leu Arg Ser Arg Arg Leu Leu Ala Tyr Met
240      115      120      125
242 Glu His Met Asn Arg Glu Tyr Arg His His Ser Leu Ala Gly Val Thr

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243      130      135      140
245 Phe Val Ser Ser His Ala Ala Phe Arg Met Ser Arg Asn Phe Thr Val
246 145      150      155      160
248 Val Trp Ile Met Ser Cys Leu Leu Gly Val Ile Ser Trp Gly Val Ser
249      165      170      175
251 Pro Leu Met Leu Gly Ile Arg Met Leu Pro Leu Gln Cys Trp Tyr Pro
252      180      185      190
254 Phe Asp Ala Leu Gly Pro Gly Thr Tyr Thr Ala Val Tyr Ala Thr Gln
255      195      200      205
257 Leu Phe Gly Gln Ile Met Val Gly Met Thr Phe Gly Phe Gly Gly Ser
258      210      215      220
260 Leu Phe Val Thr Leu Ser Leu Leu Leu Leu Gly Gln Phe Asp Val Leu
261 225      230      235      240
263 Tyr Cys Ser Leu Lys Asn Leu Asp Ala His Thr Lys Leu Leu Gly Gly
264      245      250      255
266 Glu Ser Val Asn Gly Leu Ser Ser Leu Gln Glu Glu Leu Leu Leu Gly
267      260      265      270
269 Asp Ser Lys Arg Glu Leu Asn Gln Tyr Val Leu Leu Gln Glu His Pro
270      275      280      285
272 Thr Asp Leu Leu Arg Leu Ser Ala Gly Arg Lys Cys Pro Asp Gln Gly
273      290      295      300
275 Asn Ala Phe His Asn Ala Leu Val Glu Cys Ile Arg Leu His Arg Phe
276 305      310      315      320
278 Ile Leu His Cys Ser Gln Glu Leu Glu Asn Leu Phe Ser Pro Tyr Cys
279      325      330      335
281 Leu Val Lys Ser Leu Gln Ile Thr Phe Gln Leu Cys Leu Leu Val Phe
282      340      345      350
284 Val Gly Val Ser Gly Thr Arg Glu Val Leu Arg Ile Val Asn Gln Leu
285      355      360      365
287 Gln Tyr Leu Gly Leu Thr Ile Phe Glu Leu Leu Met Phe Thr Tyr Cys
288      370      375      380
290 Gly Glu Leu Leu Ser Arg His Ser Ile Arg Ser Gly Asp Ala Phe Trp
291 385      390      395      400
293 Arg Gly Ala Trp Trp Lys His Ala His Phe Ile Arg Gln Asp Ile Leu
294      405      410      415
296 Ile Phe Leu Val Asn Ser Arg Arg Ala Val His Val Thr Ala Gly Lys
297      420      425      430
299 Phe Tyr Val Met Asp Val Asn Arg Leu Arg Ser Val Ile Thr Gln Ala
300      435      440      445
302 Phe Ser Phe Leu Thr Leu Leu Gln Lys Leu Ala Ala Lys Lys Thr Glu
303      450      455      460
305 Ser Glu Leu
306 465
308 <210> SEQ ID NO: 5
309 <211> LENGTH: 1556
310 <212> TYPE: DNA
311 <213> ORGANISM: DROSOPHILA MELANOGASTER DOR87
313 <400> SEQUENCE: 5
314 ggcacgaggc ttatagaaag tgccgagcaa tgacaatcga ggatatcggc ctggtgggca

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60

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316 tcaacgtgcg gatgtggcga cacttggccg tgctgtaccc cactccgggc tccagctggc 120
318 gcaagttcgc cttcgtgctg ccggtgactg cgatgaactc gatgcagttc gtctacctgc 180
320 tgcgagatg gggcgacctg cccgccttca ttctgaacat gttcttcttc tcggccattt 240
322 tcaacgccct gatgcgcacg tggctgggtca taatcaagcg gcgccagttc gaggagtttc 300
324 tcggccaact ggccactctg ttccattcga ttctcgactc caccgacgag tgggggcgtg 360
326 gcatcctgcg gagggcggaa cgggaggctc ggaacctggc catccttaat ttgagtcct 420
328 ccttctgga cattgtcggg gctctggtat cgccgctttt cagggaggag agagctcatc 480
330 ccttcggcgt agctctacca cggagtgcga tgaccagttc acccgtctac gaggttatct 540
332 acttggccca actgcctaag cccctgctgc tgtccatgat gtacatgcct ttcgtcagcc 600
334 tttttgccgg cctggccatc tttgggaagg ccattgctga gatcctggta cacaggctgg 660
336 gccagattgg cggagaagag cagtcggagg aggagcgctt ccaaaggctg gcctcctgca 720
338 ttgcgtacca cagcgaggtg atgcgctatg tgtggcagct caacaaactg gtggccaaca 780
340 ttgtggcggg ggaagcaatt attttggct cgataatctg ctcaactgctc ttctgtctga 840
342 atattataac ctaccccacc caggatgatc cgatagtgat gtacattctg accatgctgt 900
344 acgttctctt cactactac aatcgggcca atgaaatag cctcgagaac aaccgggtgg 960
346 cggaggctgt ttacaatgtg ccttgggtacg aggcaggaa cgggtttcgc aaaacctcc 1020
348 tgatcttctt gatgcaaa caacaccga tggagataag agtcggcaac gtttacccca 1080
350 tgacattggc catgttcacg agtctgttga atgcgtccta ctccacttt accatgctgc 1140
352 gtggcgctcac cggcaaatga gctgaaagac cgaaaaaacc ggagtatccc ctccatatt 1200
354 cccctgctc ctttattttt ctttctttt ccttttccg tttccattc gcttttccag 1260
356 caatccgggt aatgcaaaaa gttgttgctg gctgtggtcc tggctgcttg tttggcattt 1320
358 gcatatgctt gtcgtttgaa aggatttaac cggactgctg gcacggagtc ggcacctcgg 1380
360 ctctcgatc ctggcatgca aatagttggc ttcttagatt gttacacaaa atagattgta 1440
362 gattgcagct gaattgtgtg cttggaataa agtcaaaagg atgtggagtc ggcccaaggc 1500
364 tctgccatt ctgtttgctc gggatgccc aaagtatgaa aaaaaaaaa aaaaaa 1556
367 <210> SEQ ID NO: 6
368 <211> LENGTH: 376
369 <212> TYPE: PRT
370 <213> ORGANISM: DROSOPHILA MELANOGASTER DOR87
372 <400> SEQUENCE: 6
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375 1 5 10 15
377 Arg His Leu Ala Val Leu Tyr Pro Thr Pro Gly Ser Ser Trp Arg Lys
378 20 25 30
380 Phe Ala Phe Val Leu Pro Val Thr Ala Met Asn Leu Met Gln Phe Val
381 35 40 45
383 Tyr Leu Leu Arg Met Trp Gly Asp Leu Pro Ala Phe Ile Leu Asn Met
384 50 55 60
386 Phe Phe Phe Ser Ala Ile Phe Asn Ala Leu Met Arg Thr Trp Leu Val
387 65 70 75 80
389 Ile Ile Lys Arg Arg Gln Phe Glu Glu Phe Leu Gly Gln Leu Ala Thr
390 85 90 95
392 Leu Phe His Ser Ile Leu Asp Ser Thr Asp Glu Trp Gly Arg Gly Ile
393 100 105 110
395 Leu Arg Arg Ala Glu Arg Glu Ala Arg Asn Leu Ala Ile Leu Asn Leu
396 115 120 125
398 Ser Ala Ser Phe Leu Asp Ile Val Gly Ala Leu Val Ser Pro Leu Phe
399 130 135 140
401 Arg Glu Glu Arg Ala His Pro Phe Gly Val Ala Leu Pro Gly Val Ser

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\58715-A-PCT-US.txt

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L:6893 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:108